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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/919,835

DATE: 11/26/2001

TIME: 12:14:30

Input Set : A:\211710US0X.txt.

Output Set: N:\CRF3\11212001\I919835.raw

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3 <110> APPLICANT: BATHE, BRIGITTE
4      MOECKEL, BETTINA
5      PFEFFERLE, WALTER
6      HUTHMACHER, KLAUS
7      RUECKERT, CHRISTIAN
8      KALINOWSKI, JOERN
9      PUEHLER, ALFRED
10     BINDER, MICHAEL
11     GREISSINGER, DIETER
12     THIERBACH, GEORG
14 <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE METE GENE
16 <130> FILE REFERENCE: 211710US0X
18 <140> CURRENT APPLICATION NUMBER: 09/919,835
19 <141> CURRENT FILING DATE: 2001-08-02
21 <150> PRIOR APPLICATION NUMBER: DE 10038023.9
22 <151> PRIOR FILING DATE: 2000-08-02
24 <150> PRIOR APPLICATION NUMBER: DE 10109689.5
25 <151> PRIOR FILING DATE: 2001-02-28
27 <150> PRIOR APPLICATION NUMBER: US 60/294,250
28 <151> PRIOR FILING DATE: 2001-05-31
30 <160> NUMBER OF SEQ ID NOS: 8
32 <170> SOFTWARE: PatentIn version 3.1
34 <210> SEQ ID NO: 1
35 <211> LENGTH: 2810
36 <212> TYPE: DNA
37 <213> ORGANISM: Corynebacterium glutamicum
39 <220> FEATURE:
40 <221> NAME/KEY: CDS
41 <222> LOCATION: (317)..(2551)
42 <223> OTHER INFORMATION:
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50 gaggaacgcc aaagctttct gaatggaaat tttaagcggt aagtgggacg acctcgatta      180
52 caaaaaggcg aggaaacccc cggggcagct ttctgccacc cggtgatttc gcgaaccttg      240
54 aaacatcgtc agaagattgc cgtgcgtcct agccgggatc cgcacgttcg gctcaagcag      300
56 aaagtcttta actcac atg act tcc aac ttt tct tcc act gtc gct ggt ctt      352
57      Met Thr Ser Asn Phe Ser Ser Thr Val Ala Gly Leu
58      1              5              10
60 cct cgc atc gga gcg aag cgt gaa ctg aag ttc gcg ctc gaa ggc tac      400
61 Pro Arg Ile Gly Ala Lys Arg Glu Leu Lys Phe Ala Leu Glu Gly Tyr
62      15              20              25
64 tgg aat gga tca att gaa ggt cgc gaa ctt gcg cag acc gcc cgc caa      448
65 Trp Asn Gly Ser Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln
66      30              35              40
68 ttg gtc aac act gca tcg gat tct ttg tct gga ttg gat tcc gtt ccg      496
69 Leu Val Asn Thr Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro

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73	Phe Ala Gly Arg Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile				
74		65	70	75	
76	tta ggt gta ctg ccg gag cgt ttt gat gac atc gct gat cat gaa aac				592
77	Leu Gly Val Leu Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn				
78		80	85	90	
80	gat ggt ctc cca ctg tgg att gac cgc tac ttt ggc gct gct cgc ggt				640
81	Asp Gly Leu Pro Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly				
82		95	100	105	
84	act gag acc ctg cct gca cag gca atg acc aag tgg ttt gat acc aac				688
85	Thr Glu Thr Leu Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn				
86		110	115	120	
88	tac cac tac ctc gtg ccg gag ttg tct gcg gat aca cgt ttc gtt ttg				736
89	Tyr His Tyr Leu Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu				
90	125	130	135	140	
92	gat gcg tcc gcg ctg att gag gat ctc cgt tgc cag cag gtt cgt ggc				784
93	Asp Ala Ser Ala Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly				
94		145	150	155	
96	gtt aat gcc cgc cct gtt ctg gtt ggt cca ctg act ttc ctt tcc ctt				832
97	Val Asn Ala Arg Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu				
98		160	165	170	
100	gct cgc acc act gat ggt tcc aat cct ttg gat cac ctg cct gca ctg				880
101	Ala Arg Thr Thr Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu				
102		175	180	185	
104	ttt gag gtc tac gag cgc ctc atc aag tct ttc gat act gag tgg gtt				928
105	Phe Glu Val Tyr Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val				
106		190	195	200	
108	cag atc gat gag cct gcg ttg gtc acc gat gtt gct cct gag gtt ttg				976
109	Gln Ile Asp Glu Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu				
110	205	210	215	220	
112	gag cag gtc cgc gct ggt tac acc act ttg gct aag cgc gat ggc gtg				1024
113	Glu Gln Val Arg Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val				
114		225	230	235	
116	ttt gtc aat act tac ttc ggc tct ggc gat cag gcg ctg aac act ctt				1072
117	Phe Val Asn Thr Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu				
118		240	245	250	
120	gcg ggc atc ggc ctt ggc gcg att ggc gtt gac ttg gtc acc cat ggc				1120
121	Ala Gly Ile Gly Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly				
122		255	260	265	
124	gtc act gag ctt gct gcg tgg aag ggt gag gag ctg ctg gtt gcg ggc				1168
125	Val Thr Glu Leu Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly				
126		270	275	280	
128	atc gtt gat ggt cgt aac att tgg cgc acc gac ctg tgt gct gct ctt				1216
129	Ile Val Asp Gly Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu				
130	285	290	295	300	
132	gct tcc ctg aag cgc ctg gca gct cgc ggc cca atc gca gtg tct acc				1264
133	Ala Ser Leu Lys Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr				
134		305	310	315	

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136	tct	tgt	tca	ctg	ctg	cac	gtt	cct	tac	acc	ctc	gag	gct	gag	aac	att	1312
137	Ser	Cys	Ser	Leu	Leu	His	Val	Pro	Tyr	Thr	Leu	Glu	Ala	Glu	Asn	Ile	
138				320					325					330			
140	gag	cct	gag	gtc	cgc	gac	tgg	ctt	gcc	ttc	ggc	tcg	gag	aag	atc	acc	1360
141	Glu	Pro	Glu	Val	Arg	Asp	Trp	Leu	Ala	Phe	Gly	Ser	Glu	Lys	Ile	Thr	
142			335					340					345				
144	gag	gtc	aag	ctg	ctt	gcc	gac	gcc	cta	gcc	ggc	aac	atc	gac	gcg	gct	1408
145	Glu	Val	Lys	Leu	Leu	Ala	Asp	Ala	Leu	Ala	Gly	Asn	Ile	Asp	Ala	Ala	
146		350				355					360						
148	gcg	ttc	gat	gcg	gcg	tcc	gca	gca	att	gct	tct	cga	cgc	acc	tcc	cca	1456
149	Ala	Phe	Asp	Ala	Ala	Ser	Ala	Ala	Ile	Ala	Ser	Arg	Arg	Thr	Ser	Pro	
150	365					370				375						380	
152	cgc	acc	gca	cca	atc	acg	cag	gaa	ctc	cct	ggc	cgt	agc	cgt	gga	tcc	1504
153	Arg	Thr	Ala	Pro	Ile	Thr	Gln	Glu	Leu	Pro	Gly	Arg	Ser	Arg	Gly	Ser	
154				385					390					395			
156	ttc	gac	act	cgt	gtt	acg	ctg	cag	gag	aag	tca	ctg	gag	ctt	cca	gct	1552
157	Phe	Asp	Thr	Arg	Val	Thr	Leu	Gln	Glu	Lys	Ser	Leu	Glu	Leu	Pro	Ala	
158			400					405					410				
160	ctg	cca	acc	acc	acc	att	ggc	tct	ttc	cca	cag	acc	cca	tcc	att	cgt	1600
161	Leu	Pro	Thr	Thr	Thr	Ile	Gly	Ser	Phe	Pro	Gln	Thr	Pro	Ser	Ile	Arg	
162			415				420					425					
164	tct	gct	cgc	gct	cgt	ctg	cgc	aag	gaa	tcc	atc	act	ttg	gag	cag	tac	1648
165	Ser	Ala	Arg	Ala	Arg	Leu	Arg	Lys	Glu	Ser	Ile	Thr	Leu	Glu	Gln	Tyr	
166		430				435				440							
168	gaa	gag	gca	atg	cgc	gaa	gaa	atc	gat	ctg	gtc	atc	gcc	aag	cag	gaa	1696
169	Glu	Glu	Ala	Met	Arg	Glu	Glu	Ile	Asp	Leu	Val	Ile	Ala	Lys	Gln	Glu	
170	445				450			455							460		
172	gaa	ctt	ggc	ctt	gat	gtg	ttg	gtt	cac	ggc	gag	cca	gag	cgc	aac	gac	1744
173	Glu	Leu	Gly	Leu	Asp	Val	Leu	Val	His	Gly	Glu	Pro	Glu	Arg	Asn	Asp	
174				465				470					475				
176	atg	gtt	cag	tac	ttc	tct	gaa	ctt	ctc	gac	ggc	ttc	ctc	tca	acc	gcc	1792
177	Met	Val	Gln	Tyr	Phe	Ser	Glu	Leu	Leu	Asp	Gly	Phe	Leu	Ser	Thr	Ala	
178			480					485					490				
180	aac	ggc	tgg	gtc	caa	agc	tac	ggc	tcc	cgc	tgt	gtt	cgt	cct	cca	gtg	1840
181	Asn	Gly	Trp	Val	Gln	Ser	Tyr	Gly	Ser	Arg	Cys	Val	Arg	Pro	Pro	Val	
182			495					500					505				
184	ttg	ttc	gga	aac	gtt	tcc	cgc	cca	gcg	cca	atg	act	gtc	aag	tgg	ttc	1888
185	Leu	Phe	Gly	Asn	Val	Ser	Arg	Pro	Ala	Pro	Met	Thr	Val	Lys	Trp	Phe	
186		510				515					520						
188	cag	tac	gca	cag	agc	ctg	acc	cag	aag	cat	gtc	aag	gga	atg	ctc	acc	1936
189	Gln	Tyr	Ala	Gln	Ser	Leu	Thr	Gln	Lys	His	Val	Lys	Gly	Met	Leu	Thr	
190	525				530				535						540		
192	ggc	cca	gtc	acc	atc	ctt	gca	tgg	tcc	ttc	gtt	cgc	gat	gat	cag	ccg	1984
193	Gly	Pro	Val	Thr	Ile	Leu	Ala	Trp	Ser	Phe	Val	Arg	Asp	Asp	Gln	Pro	
194				545				550					555				
196	ctg	gct	acc	act	gct	gac	cag	gtt	gca	ctg	gca	ctg	cgc	gat	gaa	att	2032
197	Leu	Ala	Thr	Thr	Ala	Asp	Gln	Val	Ala	Leu	Ala	Leu	Arg	Asp	Glu	Ile	
198			560					565					570				
200	aac	gat	ctc	atc	gag	gct	ggc	gcg	aag	atc	atc	cag	gtg	gat	gag	cct	2080

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205 Ala Ile Arg Glu Leu Leu Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr
206      590      595      600
208 ctg cag tgg tcc gtg gac tcc ttc cgc ctg gcg act gcc ggc gca ccc      2176
209 Leu Gln Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro
210 605      610      615      620
212 gac gac gtc caa atc cac acc cac atg tgc tac tcc gag ttc aac gaa      2224
213 Asp Asp Val Gln Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu
214      625      630      635
216 gtg atc tcc tcc gtc atc gcg ttg gat gcc gat gtc acc acc atc gaa      2272
217 Val Ile Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu
218      640      645      650
220 gca gca cgt tcc gac atg cag gtc ctc gct gct ctg aaa tct tcc ggc      2320
221 Ala Ala Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly
222      655      660      665
224 ttc gag ctc ggc gtc gga cct ggt gtg tgg gat atc cac tcc ccg cgc      2368
225 Phe Glu Leu Gly Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg
226      670      675      680
228 gtt cct tcc gcg cag gaa gtg gac ggt ctc ctc gag gct gca ctg cag      2416
229 Val Pro Ser Ala Gln Glu Val Asp Gly Leu Leu Glu Ala Ala Leu Gln
230 685      690      695      700
232 tcc gtg gat cct cgc cag ctg tgg gtc aac cca gac tgt ggt ctg aag      2464
233 Ser Val Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys
234      705      710      715
236 acc cgt gga tgg cca gaa gtg gaa gct tcc cta aag gtt ctc gtt gag      2512
237 Thr Arg Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu
238      720      725      730
240 tcc gct aag cag gct cgt gag aaa atc gga gca act atc taaattgggt      2561
241 Ser Ala Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile
242      735      740      745
244 taccgctagg aacccaaaga ttaagggcac gagtgtcacc aggattgccg caccatggc      2621
246 aacaccgaag gacaccgtgc ccactcctat ttgcatcaca gcgcccgaagg tagcggcgcc      2681
248 caaaacagcg cccacctggc gtgaggtgtt gtaaaaacca gaagcagagc ccactaaatc      2741
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252 accgaacaa      2810
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267      20      25      30
270 Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr
271      35      40      45
274 Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg

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282	Pro	Glu	Arg	Phe	Asp	Asp	Ile	Ala	Asp	His	Glu	Asn	Asp	Gly	Leu	Pro
283					85					90					95	
286	Leu	Trp	Ile	Asp	Arg	Tyr	Phe	Gly	Ala	Ala	Arg	Gly	Thr	Glu	Thr	Leu
287				100					105					110		
290	Pro	Ala	Gln	Ala	Met	Thr	Lys	Trp	Phe	Asp	Thr	Asn	Tyr	His	Tyr	Leu
291			115					120					125			
294	Val	Pro	Glu	Leu	Ser	Ala	Asp	Thr	Arg	Phe	Val	Leu	Asp	Ala	Ser	Ala
295		130					135					140				
298	Leu	Ile	Glu	Asp	Leu	Arg	Cys	Gln	Gln	Val	Arg	Gly	Val	Asn	Ala	Arg
299	145					150					155					160
302	Pro	Val	Leu	Val	Gly	Pro	Leu	Thr	Phe	Leu	Ser	Leu	Ala	Arg	Thr	Thr
303					165					170					175	
306	Asp	Gly	Ser	Asn	Pro	Leu	Asp	His	Leu	Pro	Ala	Leu	Phe	Glu	Val	Tyr
307				180					185					190		
310	Glu	Arg	Leu	Ile	Lys	Ser	Phe	Asp	Thr	Glu	Trp	Val	Gln	Ile	Asp	Glu
311			195					200					205			
314	Pro	Ala	Leu	Val	Thr	Asp	Val	Ala	Pro	Glu	Val	Leu	Glu	Gln	Val	Arg
315		210					215					220				
318	Ala	Gly	Tyr	Thr	Thr	Leu	Ala	Lys	Arg	Asp	Gly	Val	Phe	Val	Asn	Thr
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322	Tyr	Phe	Gly	Ser	Gly	Asp	Gln	Ala	Leu	Asn	Thr	Leu	Ala	Gly	Ile	Gly
323					245					250					255	
326	Leu	Gly	Ala	Ile	Gly	Val	Asp	Leu	Val	Thr	His	Gly	Val	Thr	Glu	Leu
327				260					265					270		
330	Ala	Ala	Trp	Lys	Gly	Glu	Glu	Leu	Leu	Val	Ala	Gly	Ile	Val	Asp	Gly
331			275					280					285			
334	Arg	Asn	Ile	Trp	Arg	Thr	Asp	Leu	Cys	Ala	Ala	Leu	Ala	Ser	Leu	Lys
335		290					295					300				
338	Arg	Leu	Ala	Ala	Arg	Gly	Pro	Ile	Ala	Val	Ser	Thr	Ser	Cys	Ser	Leu
339	305					310					315					320
342	Leu	His	Val	Pro	Tyr	Thr	Leu	Glu	Ala	Glu	Asn	Ile	Glu	Pro	Glu	Val
343					325					330					335	
346	Arg	Asp	Trp	Leu	Ala	Phe	Gly	Ser	Glu	Lys	Ile	Thr	Glu	Val	Lys	Leu
347				340					345					350		
350	Leu	Ala	Asp	Ala	Leu	Ala	Gly	Asn	Ile	Asp	Ala	Ala	Ala	Phe	Asp	Ala
351			355					360					365			
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VERIFICATION SUMMARY

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